

SEQUENCE LISTING



<110> Broun, Pierre

<120> METHOD FOR MODIFYING A BIOSYNTHETIC
PATHWAY

<130> 514442001200/MBI0032

<140> US 09/810,836

<141> 2001-03-16

<160> 18

<170> FastSEQ for Windows Version 4.0

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<220>

<221> CDS

<222> (6)...(1091)

<223> G993

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ctc	tcc	atc	tct	act	act	cca	aag	ccg	aca	acg	acg	acg	gag	aag	aaa	98
Leu	Ser	Ile	Ser	Thr	Thr	Pro	Lys	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Lys	
				20					25					30		

ctc	tct	tct	ccg	ccg	gcg	acg	tcg	atg	cgt	ctc	tac	aga	atg	gga	agc	146
Leu	Ser	Ser	Pro	Pro	Ala	Thr	Ser	Met	Arg	Leu	Tyr	Arg	Met	Gly	Ser	
			35					40					45			

ggc	gga	agc	agc	gtc	gtt	ttg	gat	tca	gag	aac	ggc	gtc	gag	acc	gag	194
Gly	Gly	Ser	Ser	Val	Val	Leu	Asp	Ser	Glu	Asn	Gly	Val	Glu	Thr	Glu	
		50					55					60				

tca	cgt	aag	ctt	cct	tcg	tcg	aaa	tat	aaa	ggc	gtt	gtg	cct	cag	cct	242
Ser	Arg	Lys	Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly	Val	Val	Pro	Gln	Pro	
	65						70				75					

aac	gga	aga	tgg	gga	gct	cag	att	tac	gag	aag	cat	cag	cga	gtt	tgg	290
Asn	Gly	Arg	Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys	His	Gln	Arg	Val	Trp	
80					85					90					95	

ctc	ggt	act	ttc	aac	gag	gaa	gaa	gaa	gct	gcg	tct	tct	tac	gac	atc	338
Leu	Gly	Thr	Phe	Asn	Glu	Glu	Glu	Glu	Ala	Ala	Ser	Ser	Tyr	Asp	Ile	
			100						105					110		

gcc	gtg	agg	aga	ttc	cgc	ggc	cgc	gac	gcc	gtc	act	aac	ttc	aaa	tct	386
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Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser	
115 120 125	
caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct	434
Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser	
130 135 140	
aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag	482
Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu	
145 150 155	
ttt gag cag agt aga cgg aag ttt gtt aac ggc gac gga aaa cgc tct	530
Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser	
160 165 170 175	
ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gcg cgt	578
Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg	
180 185 190	
gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg	626
Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu	
195 200 205	
aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta	674
Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu	
210 215 220	
ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc	722
Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly	
225 230 235	
gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt	770
Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg	
240 245 250 255	
tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag ggc tgg	818
Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp	
260 265 270	
agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt	866
Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys	
275 280 285	
ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa	914
Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys	
290 295 300	
gtc cgg tct agt ccg gtt cag act gtg gtt agg cta ttc gga gtc aac	962
Val Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn	
305 310 315	
att ttc aat gtg agt aac gag aaa cca aac gac gtc gca gta gag tgt	1010
Ile Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys	
320 325 330 335	
gtt ggc aag aag aga tct cgg gaa gat gat ttg ttt tcg tta ggg tgt	1058
Val Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys	

340	345	350	
tcc aag aag cag gcg att atc aac atc ttg tga caaattcttt ttttttggtt			1111
Ser Lys Lys Gln Ala Ile Ile Asn Ile Leu *			
355	360		

tttttcttca atttgtttct cctttttcaa ttttttgat tgaaatgaca agttgtaaat	1171
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35 40 45	
Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser	
50 55 60	
Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn	
65 70 75 80	
Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu	
85 90 95	
Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala	
100 105 110	
Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln	
115 120 125	
Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys	
130 135 140	
Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe	
145 150 155 160	
Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly	
165 170 175	
Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu	
180 185 190	
Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn	
195 200 205	
Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro	
210 215 220	
Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val	
225 230 235 240	
Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr	
245 250 255	
Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser	
260 265 270	
Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe	
275 280 285	
Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val	
290 295 300	
Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile	
305 310 315 320	
Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val	

Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
 325 330 335
 340 345
 Lys Lys Gln Ala Ile Ile Asn Ile Leu
 350 355 360

aga caa cgt caa tgg gga aaa tgg gtc gca gag atc cgt aag cca cga	596
Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys Pro Arg	
150 155 160	
agc agg gca cgt ctt tgg ctt ggt acc ttt gat aca gct gaa gaa gct	644
Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala	
165 170 175	
gcc atg gcc tac gac cgc caa gcc ttc aaa tta cga ggc cac agc gca	692
Ala Met Ala Tyr Asp Arg Gln Ala Phe Lys Leu Arg Gly His Ser Ala	
180 185 190	
aca ctg aat ttc ccg gag cat ttt gtg aat aag gaa agc gag ctg cat	740
Thr Leu Asn Phe Pro Glu His Phe Val Asn Lys Glu Ser Glu Leu His	
195 200 205 210	
gat tca aac tcg tcg gat cag aaa gaa cct gaa acg cca cag cca agc	788
Asp Ser Asn Ser Ser Asp Gln Lys Glu Pro Glu Thr Pro Gln Pro Ser	
215 220 225	
gag gtt aac ttg gag agc aag gaa cta ccg gtg att gat gtt ggg aga	836
Glu Val Asn Leu Glu Ser Lys Glu Leu Pro Val Ile Asp Val Gly Arg	
230 235 240	
gag gaa ggt atg gct gag gca tgg tac aat gcc att aca tcg gga tgg	884
Glu Glu Gly Met Ala Glu Ala Trp Tyr Asn Ala Ile Thr Ser Gly Trp	
245 250 255	
ggt cct gaa agt cct ctt tgg gat gat ttg gat agt tct cat cag ttt	932
Gly Pro Glu Ser Pro Leu Trp Asp Asp Leu Asp Ser Ser His Gln Phe	
260 265 270	
tca tca gaa agc tca tct tct tct cct ctc tct tgt cct atg agg cct	980
Ser Ser Glu Ser Ser Ser Ser Ser Pro Leu Ser Cys Pro Met Arg Pro	
275 280 285 290	
ttc ttt tga aaaagtttat aaaccacat tgtgtttag gttatagttt	1029
Phe Phe *	
agggttatgc tcattggcat ttggatggag gcaatttttg tgatctccca ttccaccaca	1089
tatcagtcac tatatgtgtc taccttttct ctgtatttct atcattatca ttgtttttat	1149
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Ser Ser Ser Pro Tyr Ser Leu Glu Ala Phe Pro Phe Ser Leu Asp Pro		
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Thr Leu Gln Asn Gln Gln Gln Leu Gly Ser Tyr Val Pro Val Leu		
65	70	75
Glu Gln Arg Gln Asp Pro Thr Met Gln Gly Gln Lys Gln Met Ile Ser		80
	85	90
Phe Ser Pro Gln Gln Gln Gln Gln Gln Gln Tyr Met Ala Gln Tyr		95
	100	105
Trp Ser Asp Thr Leu Asn Leu Ser Pro Arg Gly Arg Met Met Met Met		110
	115	120
Met Ser Gln Glu Ala Val Gln Pro Tyr Ile Ala Thr Lys Leu Tyr Arg		125
	130	135
Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys		140
145	150	155
Pro Arg Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu		160
	165	170
Glu Ala Ala Met Ala Tyr Asp Arg Gln Ala Phe Lys Leu Arg Gly His		175
	180	185
Ser Ala Thr Leu Asn Phe Pro Glu His Phe Val Asn Lys Glu Ser Glu		190
	195	200
Leu His Asp Ser Asn Ser Ser Asp Gln Lys Glu Pro Glu Thr Pro Gln		205
	210	215
Pro Ser Glu Val Asn Leu Glu Ser Lys Glu Leu Pro Val Ile Asp Val		220
225	230	235
Gly Arg Glu Glu Gly Met Ala Glu Ala Trp Tyr Asn Ala Ile Thr Ser		240
	245	250
Gly Trp Gly Pro Glu Ser Pro Leu Trp Asp Asp Leu Asp Ser Ser His		255
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Gln Phe Ser Ser Glu Ser Ser Ser Ser Ser Pro Leu Ser Cys Pro Met		270
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Arg Pro Phe Phe		285
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Met Glu Arg Asp Asp Cys Arg Arg	
1	5
ttt cag gac tcg ccg gcg cag acg acg gag aga aga gtg aaa tat aaa	160
Phe Gln Asp Ser Pro Ala Gln Thr Thr Glu Arg Arg Val Lys Tyr Lys	
10	15
cca aag aag aaa aga gcc aaa gat gat gat gat gag aaa gtt gtt tcg	208
Pro Lys Lys Lys Arg Ala Lys Asp Asp Asp Glu Lys Val Val Ser	
25	30
	35
	40

aag cat cca aat ttt cga ggt gtc aga atg aga caa tgg gga aaa tgg	256
Lys His Pro Asn Phe Arg Gly Val Arg Met Arg Gln Trp Gly Lys Trp	
45 50 55	
gtg tcc gaa atc aga gag cca aaa aag aaa tca aga atc tgg ctc ggt	304
Val Ser Glu Ile Arg Glu Pro Lys Lys Lys Ser Arg Ile Trp Leu Gly	
60 65 70	
act ttc tcc acg gcg gag atg gcg gcg cgt gct cac gac gtg gca gct	352
Thr Phe Ser Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala	
75 80 85	
tta gcc atc aaa ggc ggt tct gca cat ctc aac ttc ccg gag ctc gct	400
Leu Ala Ile Lys Gly Gly Ser Ala His Leu Asn Phe Pro Glu Leu Ala	
90 95 100	
tat cac ctc cct aga cca gct agt gcc gac cct aaa gac atc caa gct	448
Tyr His Leu Pro Arg Pro Ala Ser Ala Asp Pro Lys Asp Ile Gln Ala	
105 110 115 120	
gcc gcc gcc gca gct gca gcc gct gtg gcc att gac atg gat gta gag	496
Ala Ala Ala Ala Ala Ala Ala Val Ala Ile Asp Met Asp Val Glu	
125 130 135	
acg tct tcg ccg tcg cca tct ccc aca gtt acg gaa acg tca tct ccg	544
Thr Ser Ser Pro Ser Pro Ser Pro Thr Val Thr Glu Thr Ser Ser Pro	
140 145 150	
gct atg ata gca ctc tcc gac gac gcg ttc tcc gat ctt cct gat ctc	592
Ala Met Ile Ala Leu Ser Asp Asp Ala Phe Ser Asp Leu Pro Asp Leu	
155 160 165	
ttg ctc aac gtg aac cat aac atc gat ggc ttc tgg gac tct ttt ccc	640
Leu Leu Asn Val Asn His Asn Ile Asp Gly Phe Trp Asp Ser Phe Pro	
170 175 180	
tat gaa gaa ccc ttc ctc tct caa agt tac tag aaactcaaaa ctatgctggt	693
Tyr Glu Glu Pro Phe Leu Ser Gln Ser Tyr *	
185 190	
tttgtatgta tttttgtcat gtgaccattt tttgacgtcg aaaatcaccc ggataatcca	753
aattgtatga tttattaatg gttgatgatt tttttgtgt ggaacaatgt gtatgatacg	813
taatcaaaag ttcaaaaaaa aaataaaaaa aa	845

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<212> PRT

<213> Arabidopsis thaliana

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35 40 45	

Arg Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys
 50 55 60
 Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Ser Thr Ala Glu Met Ala
 65 70 75 80
 Ala Arg Ala His Asp Val Ala Ala Leu Ala Ile Lys Gly Gly Ser Ala
 85 90 95
 His Leu Asn Phe Pro Glu Leu Ala Tyr His Leu Pro Arg Pro Ala Ser
 100 105 110
 Ala Asp Pro Lys Asp Ile Gln Ala Ala Ala Ala Ala Ala Ala Ala
 115 120 125
 Val Ala Ile Asp Met Asp Val Glu Thr Ser Ser Pro Ser Pro Ser Pro
 130 135 140
 Thr Val Thr Glu Thr Ser Ser Pro Ala Met Ile Ala Leu Ser Asp Asp
 145 150 155 160
 Ala Phe Ser Asp Leu Pro Asp Leu Leu Leu Asn Val Asn His Asn Ile
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 Met Val Lys Gln Ala Met Lys Glu Glu Glu Lys Lys Arg Asn Thr Ala
 1 5 10 15
 atg cag tca aag tac aaa gga gtg agg aag agg aaa tgg gga aaa tgg 154
 Met Gln Ser Lys Tyr Lys Gly Val Arg Lys Arg Lys Trp Gly Lys Trp
 20 25 30
 gta tcg gag atc aga ctt cca cac agc aga gaa cga att tgg tta ggc 202
 Val Ser Glu Ile Arg Leu Pro His Ser Arg Glu Arg Ile Trp Leu Gly
 35 40 45
 tct tac gac act ccc gag aag gcg gcg cgt gct ttc gac gcc gct caa 250
 Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala Gln
 50 55 60
 ttt tgt ctc cgc ggc ggc gat gct aat ttc aat ttc cct aat aat cca 298
 Phe Cys Leu Arg Gly Gly Asp Ala Asn Phe Asn Phe Pro Asn Asn Pro
 65 70 75 80
 ccg tcg atc tcc gta gaa aag tcg ttg acg cct ccg gag att cag gaa 346
 Pro Ser Ile Ser Val Glu Lys Ser Leu Thr Pro Pro Glu Ile Gln Glu
 85 90 95

gct gct gct aga ttc gct aac aca ttc caa gac att gtc aag gga gaa 394
Ala Ala Ala Arg Phe Ala Asn Thr Phe Gln Asp Ile Val Lys Gly Glu
100 105 110

gaa gaa tcg ggt tta gta ccc gga tcc gag atc cga cca gag tct cct 442
Glu Glu Ser Gly Leu Val Pro Gly Ser Glu Ile Arg Pro Glu Ser Pro
115 120 125

tct aca tct gca tct gtt gct aca tcg acg gtg gat tat gat ttt tcg 490
Ser Thr Ser Ala Ser Val Ala Thr Ser Thr Val Asp Tyr Asp Phe Ser
130 135 140

ttt ttg gat ttg ctt ccg atg aat ttc ggg ttt gat tcc ttc tcc gac 538
Phe Leu Asp Leu Leu Pro Met Asn Phe Gly Phe Asp Ser Phe Ser Asp
145 150 155 160

gac ttc tct ggc ttc tcc ggt ggt gat cga ttt aca gag att tta ccc 586
Asp Phe Ser Gly Phe Ser Gly Gly Asp Arg Phe Thr Glu Ile Leu Pro
165 170 175

atc gaa gat tac gga gga gag agt tta tta gat gaa tct ttg att ctt 634
Ile Glu Asp Tyr Gly Gly Glu Ser Leu Leu Asp Glu Ser Leu Ile Leu
180 185 190

tgg gat ttt tga attcccaaac ataatatattt tttagagcga actgtgagat 686
Trp Asp Phe *
195

tttccttgga gtcattggaga aatctggaga ttttttgtaa cacggagctc caatgaccgcg 746
ggaatttctt tcgtttcgga tccgaatttg atgtggatca tattcacacc tatatttttt 806
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35 40 45
Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala Gln
50 55 60
Phe Cys Leu Arg Gly Gly Asp Ala Asn Phe Asn Phe Pro Asn Asn Pro
65 70 75 80
Pro Ser Ile Ser Val Glu Lys Ser Leu Thr Pro Pro Glu Ile Gln Glu
85 90 95
Ala Ala Ala Arg Phe Ala Asn Thr Phe Gln Asp Ile Val Lys Gly Glu
100 105 110
Glu Glu Ser Gly Leu Val Pro Gly Ser Glu Ile Arg Pro Glu Ser Pro
115 120 125
Ser Thr Ser Ala Ser Val Ala Thr Ser Thr Val Asp Tyr Asp Phe Ser
130 135 140

Phe Leu Asp Leu Leu Pro Met Asn Phe Gly Phe Asp Ser Phe Ser Asp
 145 150 155 160
 Asp Phe Ser Gly Phe Ser Gly Gly Asp Arg Phe Thr Glu Ile Leu Pro
 165 170 175
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 180 185 190
 Trp Asp Phe
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<210> 9
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 cgcggatccg ccaggagagt tggtgattca ttgtttgc 38

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<210> 18
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cgcggaacca ttaatctttc cttccgctct ctttctatg

39